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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/028,247

DATE: 04/01/2002

TIME: 15:24:52

Input Set : A:\-335-2.app

Output Set: N:\CRF3\04012002\J028247.raw

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3 <110> APPLICANT: Goldman, Stanley
4      Lathrop, Stephanie J.
5      Longchamp, Pascal F.
6      Whalen, Robert G.
7      Maxygen, Inc.
9 <120> TITLE OF INVENTION: Methods and Compositions for Developing Spore Display
10     Systems for Medicinal and Industrial Applications
12 <130> FILE REFERENCE: 18097A-033520US
14 <140> CURRENT APPLICATION NUMBER: US 10/028,247
15 <141> CURRENT FILING DATE: 2001-12-19
17 <150> PRIOR APPLICATION NUMBER: US 60/214,161
18 <151> PRIOR FILING DATE: 2000-06-26
20 <150> PRIOR APPLICATION NUMBER: US 09/892,208
21 <151> PRIOR FILING DATE: 2001-06-26
23 <160> NUMBER OF SEQ ID NOS: 6
25 <170> SOFTWARE: PatentIn Ver. 2.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 258
29 <212> TYPE: DNA
30 <213> ORGANISM: Bacillus subtilis
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(258)
35 <223> OTHER INFORMATION: CotC27 including HA11 epitope region
37 <400> SEQUENCE: 1
38 atg ggt tat tac aaa aaa tac aaa gaa gag tat tat acg gtc aaa aaa      48
39 Met Gly Tyr Tyr Lys Lys Tyr Lys Glu Glu Tyr Tyr Thr Val Lys Lys
40   1               5               10               15
42 acg tat tat aag aag tat tac gaa tat gat aaa tct aga ggt acc tgc      96
43 Thr Tyr Tyr Lys Lys Tyr Tyr Glu Tyr Asp Lys Ser Arg Gly Thr Cys
44   20               25               30
46 tat cct tat gat gtt cct gat tat gct tct tta gga tcc ctg cag aaa      144
47 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Gly Ser Leu Gln Lys
48   35               40               45
50 gat tat gac tgt gat tac gac aaa aaa tat gat gac tat gat aaa aaa      192
51 Asp Tyr Asp Cys Asp Tyr Asp Lys Lys Tyr Asp Asp Tyr Asp Lys Lys
52   50               55               60
54 tat tat gat cac gat aaa aaa gac tat gat tat gtt gta gag tat aaa      240
55 Tyr Tyr Asp His Asp Lys Lys Asp Tyr Asp Tyr Val Val Glu Tyr Lys
56  65               70               75               80
58 aag cat aaa aaa cac tac
59 Lys His Lys Lys His Tyr
60               85

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63 <210> SEQ ID NO: 2
64 <211> LENGTH: 86
65 <212> TYPE: PRT
66 <213> ORGANISM: Bacillus subtilis
68 <220> FEATURE:
69 <223> OTHER INFORMATION: CotC27 including HA11 epitope region
71 <400> SEQUENCE: 2
72 Met Gly Tyr Tyr Lys Lys Tyr Lys Glu Glu Tyr Tyr Thr Val Lys Lys
73   1           5           10           15
74 Thr Tyr Tyr Lys Lys Tyr Tyr Glu Tyr Asp Lys Ser Arg Gly Thr Cys
75           20           25           30
76 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Leu Gly Ser Leu Gln Lys
77           35           40           45
78 Asp Tyr Asp Cys Asp Tyr Asp Lys Lys Tyr Asp Asp Tyr Asp Lys Lys
79           50           55           60
80 Tyr Tyr Asp His Asp Lys Lys Asp Tyr Asp Tyr Val Val Glu Tyr Lys
81   65           70           75           80
82 Lys His Lys Lys His Tyr
83           85
86 <210> SEQ ID NO: 3
87 <211> LENGTH: 639
88 <212> TYPE: DNA
89 <213> ORGANISM: Bacillus circulans
91 <220> FEATURE:
92 <221> NAME/KEY: CDS
93 <222> LOCATION: (1)..(639)
94 <223> OTHER INFORMATION: lipase 396
96 <400> SEQUENCE: 3
97 atg aaa ttt ata aaa aga agg atc att gca ctt gta aca att ttg gtg 48
98 Met Lys Phe Ile Lys Arg Arg Ile Ile Ala Leu Val Thr Ile Leu Val
99   1           5           10           15
101 ctg tca gtc aca tcg ctg ttt gcg atg cag ccg tca gca aaa gcc gct 96
102 Leu Ser Val Thr Ser Leu Phe Ala Met Gln Pro Ser Ala Lys Ala Ala
103           20           25           30
105 gaa cac aat cca gtt gtt atg gtt cac ggt atc gga gga gct tca tac 144
106 Glu His Asn Pro Val Val Met Val His Gly Ile Gly Gly Ala Ser Tyr
107           35           40           45
109 aat ttt gcg gga att aag agc tat ctc gta tct cag ggc tgg tca cgg 192
110 Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp Ser Arg
111           50           55           60
113 ggc aag ctg tat gcg gtt gat ttt tgg gac aag aca ggg acg aat tat 240
114 Gly Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr Asn Tyr
115   65           70           75           80
117 aac aat ggc ccg gta tta tca cga ttt gtg caa aag gtt tta gac gaa 288
118 Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu Asp Glu
119           85           90           95
121 acg ggt gcg aaa aaa gtg gat att gtc gct cac agc atg ggt ggc gcg 336
122 Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly Gly Ala
123           100           105           110

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125 aac aca ctt tac tac ata aaa aat ctg gac ggc gga aat aaa att gaa 384
126 Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys Ile Glu
127      115      120      125
129 aac gtc gta acg ctt ggc ggc gcg aac cgt ttg acg aca agc aag gcg 432
130 Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Ser Lys Ala
131      130      135      140
133 ctt ccg gga aca gat cca aat caa aag att tta tac aca tcc att tac 480
134 Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser Ile Tyr
135 145      150      155      160
137 agc agt gcc gat atg att gtc atg aat tac tta tca aaa tta gac ggt 528
138 Ser Ser Ala Asp Met Ile Val Met Asn Tyr Leu Ser Lys Leu Asp Gly
139      165      170      175
141 gct aaa aac gtt caa att cat ggc gtt ggg cac att ggt tta ttg atg 576
142 Ala Lys Asn Val Gln Ile His Gly Val Gly His Ile Gly Leu Leu Met
143      180      185      190
145 aac agc caa gtc aac agc ctg att aaa gaa gga ctg aac ggc ggc ggc 624
146 Asn Ser Gln Val Asn Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly Gly
147      195      200      205
149 ctc aat aca aat taa 639
150 Leu Asn Thr Asn
151      210
154 <210> SEQ ID NO: 4
155 <211> LENGTH: 212
156 <212> TYPE: PRT
157 <213> ORGANISM: Bacillus circulans
159 <220> FEATURE:
160 <223> OTHER INFORMATION: lipase 396
162 <400> SEQUENCE: 4
163 Met Lys Phe Ile Lys Arg Arg Ile Ile Ala Leu Val Thr Ile Leu Val
164 1 5 10 15
165 Leu Ser Val Thr Ser Leu Phe Ala Met Gln Pro Ser Ala Lys Ala Ala
166 20 25 30
167 Glu His Asn Pro Val Val Met Val His Gly Ile Gly Gly Ala Ser Tyr
168 35 40 45
169 Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp Ser Arg
170 50 55 60
171 Gly Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr Asn Tyr
172 65 70 75 80
173 Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu Asp Glu
174 85 90 95
175 Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly Gly Ala
176 100 105 110
177 Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys Ile Glu
178 115 120 125
179 Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Ser Lys Ala
180 130 135 140
181 Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser Ile Tyr
182 145 150 155 160
183 Ser Ser Ala Asp Met Ile Val Met Asn Tyr Leu Ser Lys Leu Asp Gly

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184          165          170          175
185 Ala Lys Asn Val Gln Ile His Gly Val Gly His Ile Gly Leu Leu Met
186          180          185          190
187 Asn Ser Gln Val Asn Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly Gly
188          195          200          205
189 Leu Asn Thr Asn
190          210
193 <210> SEQ ID NO: 5
194 <211> LENGTH: 29
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Description of Artificial Sequence:primer for
200      fusion protein
202 <400> SEQUENCE: 5
203 atatctgcag atttgtattg aggcccccg                29
206 <210> SEQ ID NO: 6
207 <211> LENGTH: 32
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Description of Artificial Sequence:primer for
213      terminator
215 <400> SEQUENCE: 6
216 atatctgcag ttaatttgta ttgaggcccc cg                32

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VERIFICATION SUMMARY

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